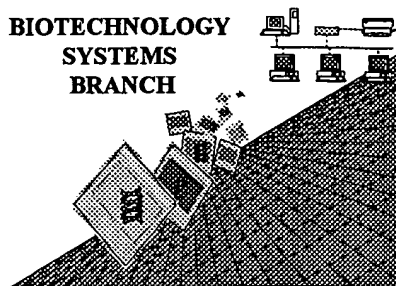


Railay

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/846,606A

Art Unit / Team No. : 1636

Date Processed by STIC: 4/14/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Railway

1636

#8 1/2

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/846,606A

DATE: 04/14/98
TIME: 13:25:10

INPUT SET: S24919.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Schering Corporation

(ii) TITLE OF INVENTION: Thioredoxin/Heterologous Protein Bacterial Expression

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Schering-Plough Corporation

(B) STREET: 2000 Galloping Hill Road

(C) CITY: Kenilworth

(D) STATE: New Jersey

(E) COUNTRY: U.S.A.

(F) ZIP : 07033-0530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: diskette

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: Macintosh 7.5.3

(D) SOFTWARE: Microsoft Word 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 60/011,606

(B) FILING DATE: 30-APR-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Thampoe, Immac J..

(B) REGISTRATION NUMBER: 36,322

(C) REFERENCE DOCKET NUMBER: JB0600Q

ERRORED SEQUENCES FOLLOW:

106 (2) INFORMATION FOR SEQ ID NO:6:

107 (i) SEQUENCE CHARACTERISTICS:

108 (A) LENGTH: 27 amino acids

109 (B) TYPE: amino acid

110 (ii) MOLECULE TYPE: peptide

111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

112

113

114 Asp Asn Asn Leu Ala Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys

115 1 5 10 15

--> (D) TOPOLOGY: mandatory leading AND
response
for ALL
types of
sequences

RAW SEQUENCE LISTING

PATENT APPLICATION US/08/846,606A

 DATE: 04/14/98
 TIME: 13:25:12

INPUT SET: S24919.raw

116
 117 Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu
 118 20 25
 119
 120

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

--> 162 (xi) SEQUENCE DESCRIPTION: (10) SEQ ID NO: 10: (repetitive error)

163

164 AAGGAGGTTT AATG 14

165

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

--> 171 (xi) SEQUENCE DESCRIPTION: (11) SEQ ID NO: 11:

172

173 Leu Asp Ala Asn Leu Ala

174

5

NUMBER AMINO ACIDS UNDER EVERY 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

--> 182 (xi) SEQUENCE DESCRIPTION: (12)

183

184 CTC GAT GCT AAT CTG GCG TAA 21

--> 185 Leu Asp Ala Asn Leu Ala

186

187

 misaligned amino acids - Please align them and
 number under every 5 amino acids

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

--> 195 (xi) SEQUENCE DESCRIPTION: (13)

196

197 CTC GAG GCT AAT CTG GCG TAA 21

--> 198 Leu Glu Ala Asn Leu Ala

6

align and number them

INPUT SET: S24919.raw

199

200 (2) INFORMATION FOR SEQ ID NO:14:

201 (i) SEQUENCE CHARACTERISTICS:

202 (A) LENGTH: 6 amino acids

203 (B) TYPE: amino acid

204 (ii) MOLECULE TYPE: peptide

205 (xi) SEQUENCE DESCRIPTION:14:

206

207 Leu Glu Ala Asn Leu Ala

208

209

210

211

→ (D) TOPOLOGY:

6

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/846,606A

DATE: 04/14/98

TIME: 13:25:15

INPUT SET: S24919.raw

Line	Error	Original Text
111	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
162	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:10:
171	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:11:
171	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION SEQ ID NO:11:
177	Entered (21) and Calc. Seq. Length (32) differ	(A) LENGTH: 21 bases
182	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:12:
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	# of Sequences for line conflicts w/ running total	Leu Asp Ala Asn Leu Ala
190	Entered (21) and Calc. Seq. Length (32) differ	(A) LENGTH: 21 bases
195	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:13:
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	# of Sequences for line conflicts w/ running total	Leu Glu Ala Asn Leu Ala
205	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:14:
205	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION SEQ ID NO:14: